IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Lorin R. DeBonte et al.   Art Unit: 1649
Serial No.: 08/572,027   Examiner: G. Benzion
Filed   : December, 14, 1995
Title   : PLANTS HAVING MUTANT SEQUENCES THAT CONFER ALTERED
            FATTY ACID PROFILES

Assistant Commissioner for Patents
Washington, DC 20231

<u>DECLARATION UNDER 37 CFR §1.132 OF GUO-HUA MIAO</u>

I, Guo-Hua Miao, declare as follows:

1.   That I am a citizen of the People's Republic of China and presently live at 202 Cherry Blossom Place, Hockessin, Delaware.

2.   That I received a Bachelor of Science degree in Biology from Shanghai Normal University, Shanghai, China in 1982, a Master of Science degree in Plant Physiology from Shanghai Institute of Plant Physiology, Chinese Academy of Science, Shanghai, China in 1984 and a Doctor of Philosophy degree in Molecular, Cellular and Developmental Biology from Ohio State University, Columbus, Ohio in 1991.

3.   That I was employed as a research associate at the Biotechnology Center, Ohio State University, Columbus, Ohio from 1991 to 1993.

4.   That I am presently employed as a Senior Research Molecular Biologist by DuPont Agricultural Products, a division of E. I. Dupont de Nemours, Inc. and have been so employed since 1993.

5.   That, as an employee of DuPont, I determined Fad2 desaturase coding sequences obtained from canola lines Westar and Q508. Westar is a canola variety having no known mutations in

Fad2 desaturase genes. Q508 is a line derived from Westar by mutagenesis. A copy of four microfilmed pages from my laboratory notebook is attached as Exhibit A (Notebook F79066, pages 140-143). These notebook pages show the DNA sequences and deduced amino acid sequences that were obtained by me or under my supervision. The dates on these four pages, all of which are prior to December 14, 1995, have been blocked out.

The DNA and deduced amino acid sequence of Fad2-F from line Q508 is shown at pages 140-141. The Q508 Fad2-F sequence contains a mutation at nucleotide 515 compared to the wild-type Westar sequence, as indicated at page 140 of the notebook. The wild-type nucleotide at this position is T, and the mutant nucleotide is A. Based on the information at pages 140-141, the mutant Q508 Fad2-F and wild-type Fad2-F sequences contain a G at position 316.

The DNA and deduced amino acid sequences of Fad2-D from the Westar variety is shown at pages 142-143. The wild-type Fad2-D sequence contains a G at nucleotide 316, whereas the IMC 129 mutant Fad2-D sequence contains an A, as indicated at page 142 of the notebook. Based on the information at pages 142-143, the wild-type Fad2-D and mutant IMC 129 Fad2-D sequences contain a T at position 515.

6. After these sequences were determined, the mutant Fad2-D sequence and the mutant Fad2-F sequence were mailed to Ronald Lundquist. A copy of the sequences that were mailed, as well as the cover letter, are attached hereto as Exhibit B. The dates on these pages, all of which are prior to December 14, 1995, have been blocked out. A comparison of the nucleotide sequences in my laboratory notebook to those enclosed with the letter to Ronald Lundquist indicates that the sequences enclosed in the letter were incorrectly labeled. The sequence labeled as "f-gene, 508" corresponds to the wild-type Fad2-D sequence of my

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notebook, with the Q508 mutation inserted at position 515. The
sequence labeled as "d-gene, 129" corresponds to the wild-type
Fad2-F sequence of my notebook, with the IMC 129 mutation
inserted at position 316. It appears that the sequence labels
were inadvertently switched and the D and F mutations added to
the sequence prior to mailing the information to Mr. Lundquist.

7.   I further declare that all statements made herein
of my own knowledge are true and that all statements made on
information and belief are believed to be true; and further that
these statements were made with the knowledge that willful false
statements and the like so made are punishable by fine or
imprisonment or both, under Section 1001 of Title 18 of the
United States Code and that such willful false statements may
jeopardize the validity of the instant patent application or any
patent issuing thereon.

Dated:_____   _____
                                       Guo-Hua Miao, Ph.D.

14066.M11

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        5      10     15     20     25     30     35     40     45
ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT
TAC CCA CGT CCA CCT TCT TAC GTT CAC AGA GGA GGG AGG TTC TTC AGA
 M   G   A   G   G   R   M   Q   V   S   P   P   S   K   K   S>

 50     55     60     65     70     75     80     85     90     95
GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT
CTT TGG CTG TGG TAG TTC GCG CAT GGG ACG CTC TGT GGC GGG AAG TGA
 E   T   D   T   I   K   R   V   P   C   E   T   P   P   F   T>

100    105    110    115    120    125    130    135    140
GTC GCA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG
CAG CCT CTT GAG TTC TTT CGT TAG GGT GGC GTG ACA AAG TTT GCG AGC
 V   G   E   L   K   K   A   I   P   P   H   C   F   K   R   S>

145    150    155    160    165    170    175    180    185    190
ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC
TAG GGA GCG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAG TAT CGG AGG
 I   P   R   S   F   S   Y   L   I   W   D   I   I   I   A   S>

195    200    205    210    215    220    225    230    235    240
TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT
ACG AAG ATG ATG NAG CGG TGG TGA ATG AAG GGA GAG GGA GTG GTG GGA
 C   F   Y   Y   X   A   T   T   Y   F   P   L   L   P   H   P>

245    250    255    260    265    270    275    280    285
CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC
GAG AGG ATG AAG CGG ACC GGA GAG ATG ACC CGG ACG GTT CCC ACG CAG
 L   S   Y   F   A   W   P   L   Y   W   A   C  ▓▓▓▓▓▓▓▓

290    295    300    305    310    315    320    325    330    335
CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC CAC GCC TTC
GAT TGG CCG CAG ACC CAG TAT CGG GTG CTC ACG CCG GTG GTG CGG AAG
 L  ▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓▓

340    345    350    355    360    365    370    375    380
AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC
TCG CTG ATG GTC ACC GAA CTG CTG TGG CAG CCA GAG TAG AAG GTG AGG
 S   D   Y   Q   W   L   D   D   T   V   G   L   I   F   H   S>

385    390    395    400    405    410    415    420    425    430
TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC
AAG GAG GAG CAG GGA ATG AAG AGG ACC TTC ATG TCA GTA GCG TCG GTG
 F   L   L   V   P   Y   F   S   W   K   Y   S   H   R   S   H>

435    440    445    450    455    460    465    470    475    480
CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG
GTA AGG TTG TGA CCG AGG GAG CTC TCT CTG CTT CAC AAG CAG GGG TTC
 H   S   N   T   G   S   L   E   R   D   E   V   F   V   P   K>

485    490    495    500    505    510        515    520    525
                                          (L)→ N→ ←129
                                          CTC
AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CAC AAC AAC CCT TTG
TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GTG TTG TTG GGA AAC
 K   K   S   D   I   K   W   Y   G   K   Y   H   N   N   P   L>

530    535    540    545    550    555    560    565    570    575
GGA CGC ACC GTG ATG TTA ACG GTT CAC TTC ACT CTC GGC TGC CCG TTG
CCT GCG TGG CAC TAC AAT TGC CAA GTC AAG TGA CAC CCG ACC GGC AAC
 G   R   T   V   M   L   T   V   Q   F   T   L   G   W   P   L>

580    585    590    595    600    605    610    615    620
TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT
ATG AAT CGG AAG TTG CAG AGC CCT TCT GGA ATG CTG CCG CCG AAG GCA
 Y   L   A   P   N   V   S   G   R   P   Y   D   G   G   F   R>
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DNA and deduced protein sequence of camba F002 (P) from Q508.

CTC was found in western and 129 clones. Thus in Q508 a histidine was replaces leucine position 514-516 bp.

this mutation B in P clone is specific to (leucine) Q508

Sequence in this region was confirmed from both strands.

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        625   630   635   640   645   650   655   660   665   670
        TCC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC
        ACG GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG
         C   H   F   H   P   N   A   P   I   Y   N   D   R   E   R   L>

        675   680   685   690   695   700   705   710   715   720
        CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC
        GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CGG CAG ACG ATG CCA GAG
         Q   I   Y   I   S   D   A   G   I   L   A   V   C   Y   G   L>

            725   730   735   740   745   750   755   760   765
        TTC CGT TAC GCC GCC GGC CAG GGA GTG GCC TCG ATG GTC TGC TTC TAC
        AAG GCA ATG CGG CGG CCG GTC CCT CAC CGG AGC TAC CAG ACG AAG ATG
         F   R   Y   A   A   G   Q   G   V   A   S   W   V   C   F   Y>

        770   775   780   785   790   795   800   805   810   815
        GGA GTC CCG CTT CTG ATT GTC AAT GGT TTC CTC GTG TTG ATC ACT TAC
        CCT CAG GGC GAA GAC TAA CAG TTA CCA AAG GAG CAC AAC TAG TGA ATG
         G   V   P   L   L   I   V   N   G   F   L   V   L   I   T   Y>

        820   825   830   835   840   845   850   855   860
        TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG
        AAC GTC GTG TGC GTA GGA AGG GAC GGA GTG ATG CTA AGC AGG CTC ACC
         L   Q   H   T   H   P   S   L   P   H   Y   D   S   S   E   W>

        865   870   875   880   885   890   895   900   905   910
        GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC
        CTA ACC AAG TCC CCT CGA AAC CGA TGG CAA CTG TCT CTG ATG CCT TAG
         D   W   F   R   G   A   L   A   T   V   D   R   D   Y   G   I>

        915   920   925   930   935   940   945   950   955   960
        TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC AUG CAC GTG GCC CAT CAT
        AAC TTG TTC CAG AAG GTG TTA TAA TGG CTG TGC GTG CAC CGG GTA GTA
         L   N   K   V   F   H   N   I   T   D   T   H   V   A   H   H>

        965   970   975   980   985   990   995  1000  1005
        CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG
        GGC AAG AGG TGC TAC GGC GTA ATA GTC CGC TAC CTT CGA TGG TTC CGC
         P   F   S   T   M   P   H   Y   H   A   M   E   A   T   K   A>

       1010  1015  1020  1025  1030  1035  1040  1045  1050  1055
        ATA AAG CCG ATA CTG GGA CAC TAT TAT CAG TTC GAT GGG ACG CCG GTG
        TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAG CTA CCC TGC GGC CAC
         I   K   P   I   L   G   E   Y   Y   Q   F   D   G   T   P   V>

       1060  1065  1070  1075  1080  1085  1090  1095  1100
        GTT AAG GCG ATG TGG AGG GAG GCG AAG GAC TGT ATC TAT GTG GAA CCG
        CAA TTC CGC TAC ACC TCC CTC CGC TTC CTG ACA TAG ATA CAC CTT GGC
         V   K   A   M   W   R   E   A   K   E   C   I   Y   V   E   P>

       1105  1110  1115  1120  1125  1130  1135  1140  1145  1150
        CAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA
        GTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT
         D   R   Q   G   E   K   K   G   V   F   W   Y   N   N   K   L>

       1155  1160  1165  1170  1175  1180  1185
        TGA GGA TAT GAT GAT GGT GAA AGA AAT CAC TAG
        ACT CCT ATA CTA CTA CCA CTT TCT TTA GTG ATC
         *   G   Y   D   D   G   E   R   N   H   *>
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See primer location on page 134.

to Q508

a MaI st was last kind on the sequence analysis.

CCTC (wt +129)
CCAC (Q508)

MaI site (CCTC)

Therefore, MaI will provide a simple way to distinguish Q508 and WC +129.

EXPERIMENTER _____ [signature] _____ DATE _____

WITNESSED BY _____ [signature] _____ DATE _____

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                5      10      15      20      25      30      35      40      45
        ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT
        TAC CCA CGT CCA CCT TCT TAC GTT CAC AGA GGA GGG AGG TTT TTC AGA
        M   G   A   G   G   R   M   Q   V   S   P   P   S   K   K   S>

        50      55      60      65      70      75      80      85      90      95
        GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT
        CTT TGG CTG TTG TAG TTC GCG CAT GGG ACG CTC TGT GGC GGG AAG TGA
        E   T   D   N   I   K   R   V   P   C   E   T   P   P   F   T>

           100     105     110     115     120     125     130     135     140
        GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG
        CAG CCT CTT GAG TTC TTT CGT TAG GGT GGC GTG ACA AAG TTT GCG AGC
        V   G   E   L   K   K   A   I   P   P   H   C   F   K   R   S>

        145     150     155     160     165     170     175     180     185     190
        ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC
        TAG GGA GCG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAG TAT CGG AGG
        I   P   R   S   F   S   Y   L   I   W   D   I   I   I   A   S>

        195     200     205     210     215     220     225     230     235     240
        TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT
        ACG AAG ATG ATG CAG CGG TGG TGA ATG AAG GGA GAG GAG GGA GTG GGA
        C   F   Y   Y   V   A   T   T   Y   F   P   L   L   P   H   P>

        245     250     255     260     265     270     275     280     285
        CTC TCC TAC TTC GCC TGC CCT CTC TAC TGG GCC TGC CAG GGC TCC GTC
        GAG AGG ATG AAG CGG ACG GGA GAG ATG ACC CGG ACG GTC CCG ACG CAG
        L   S   Y   F   A   W   P   L   Y   W   A   C   ▮▮▮▮▮▮▮▮>

        290     295     300     305     310     315     320     325     330     335
                                                A   (CK)  325 → 129, Q508
        CTA ACC GGC GTC TGG GTC ATA GCC CAC GAC TGC GGC CAC CAC GGC TTC
        GAT TGG CCG CAG ACC CAG TAT CGG GTG CTG ACG CCG GTG GTG CCG AAG
        ▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮

        340     345     350     355     360     365     370     375     380
        AGC GAC TAC CAC TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC
        TCG CTG ATG GTC ACC GAC CTG CTG TGG CAG CCG GAG TAG AAG GTG AGG
        ▮▮▮▮▮▮▮▮▮▮▮▮▮▮▮ D   T   V   G   L   I   F   H   S>

        385     390     395     400     405     410     415     420     425     430
        TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC
        AAG GAG GAG CAG GGA ATG AAG AGG ACC TTC ATG TCA GTA GCT GCG CTG
        F   L   L   V   P   Y   F   S   W   K   Y   S   H   R   R   H>

        435     440     445     450     455     460     465     470     475     480
        CAT TCC AAC ACT GGC TTC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG
        GTA AGG TTG TGA CCG AAG GAG CTC TCT CTG CTT CAC AAA CAG GGG TTC
        H   S   N   T   G   S   L   E   R   D   E   V   F   V   P   K>

        485     490     495     500     505     510     515     520     525
        AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG
        TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GAG TTG TTG GGA AAC
        K   K   S   D   I   K   W   Y   G   K   Y   L   N   N   P   L>

        530     535     540     545     550     555     560     565     570     575
        GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG
        CCT GCG TGG CAC TAC AAT TGC CAA GTC AAG TGA GAG CCG ACC GGA AAC
        G   R   T   V   M   L   T   V   Q   F   T   L   G   W   P   L>

        580     585     590     595     600     605     610     615     620
        TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT
        ATG AAT CGG AAG TTG CAG AGC CCC TCT GGA ATG CTG CCG CCG AAG CGA
        Y   L   A   F   N   V   S   G   R   P   Y   D   G   G   F   A>
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DNA and deduced protein sequence from western FAD2 (B) clone

In 129 and Q508 clones (E) (A was converted to Arg (k). This mutation was found in F clone only. So but occur in both 129 and Q508 mutant lines

Again, this region was confirmed from

EXPERIMENTER _____ [signature] _____ DATE _____

WITNESSED BY _____ [signature] _____ DATE _____

```
      625   630   635   640   645   650   655   660   665   670
      TCC   CAT   TTC   CAC   CCC   AAC   GCT   CCC   ATC   TAC   AAC   GAC   CGC   GAG   CGT   CTC
      ACG   GTA   AAG   GTG   GGG   TTG   CGA   GGG   TAG   ATG   TTG   CTG   GCG   CTC   GCA   GAG
       C     H     F     H     P     N     A     P     I     Y     N     D     R     E     R     L>

      675   680         685   690         695         700   705         710         715         720
      CAG   ATA   TAC   ATC   TCC   GAC   GCT   GGC   ATC   CTC   GCC   GTC   TGC   TAC   GGT   CTC
      GTC   TAT   ATG   TAG   AGG   CTG   CGA   CCG   TAG   GAG   CGG   CAG   ACG   ATG   CCA   GAG
       Q     I     Y     I     S     D     A     G     I     L     A     V     C     Y     G     L>

            725         730   735   740         745   750         755   760         765
      TAC   CGC   TAC   GCT   GCT   GTC   CAA   GGA   GTT   GCC   TCG   ATG   GTC   TGC   TTC   TAC
      ATG   GCG   ATG   CGA   CGA   CAG   GTT   CCT   CAA   CGG   AGC   TAC   CAG   ACG   AAG   ATG
       Y     R     Y     A     A     V     Q     G     V     A     S     M     V     C     F     Y>

      770   775   780         785         790   795         800         805   810         815
      GGA   GTT   CCG   CTT   CTG   ATT   GTC   AAT   GGG   TTC   TTA   GTT   TTG   ATC   ACT   TAC
      CCT   CAA   GGC   GAA   GAC   TAA   CAG   TTA   CCC   AAG   AAT   CAA   AAC   TAG   TGA   ATG
       G     V     P     L     L     I     V     N     G     F     L     V     L     I     T     Y>

      820   825         830   835   840         845         850   855         860
      TTG   CAG   CAC   ACG   CAT   CCT   TCC   CTG   CCT   CAC   TAT   GAC   TCG   TCT   GAG   TGG
      AAC   GTC   GTG   TGC   GTA   GGA   AGG   GAC   GGA   GTG   ATA   CTG   AGC   AGA   CTC   ACC
       L     Q     H     T     H     P     S     L     P     H     Y     D     S     S     E     W>

865         870   875         880   885         890   895   900         905   910
      GAT   TGG   TTG   AGC   GGA   GCT   TTC   GCC   ACC   GTT   GAC   AGA   GAC   TAC   GGA   ATC
      CTA   ACC   AAC   TCG   CCT   CGA   AAC   CGG   TGC   CAA   CTG   TCT   CTG   ATG   CCT   TAG
       D     W     L     R     G     A     L     A     T     V     D     R     D     Y     G     I>

      915   920         925   930   935         940   945         950   955         960
      TTG   AAC   AAG   GTC   TTC   CAC   AAT   ATC   ACC   GAC   ACG   CAC   GTG   GCG   CAT   CAC
      AAC   TTG   TTC   CAG   AAG   GTG   TTA   TAG   TGC   CTG   TGC   GTG   CAC   CGC   GTA   GTG
       L     N     K     V     F     H     N     I     T     D     T     H     V     A     H     H>

            965   970   975         980         985   990         995   1000  1005
      CTG   TTC   TCG   ACC   ATG   CCG   CAT   TAT   CAT   GCG   ATG   GAA   GCT   ACG   AAG   GCG
      GAC   AAG   AGC   TGG   TAC   GGC   GTA   ATA   GTA   CGC   TAC   CTT   CGA   TGC   TTC   CGC
       L     F     S     T     M     P     H     Y     H     A     M     E     A     T     K     A>

      1010       1015  1020       1025       1030  1035       1040       1045  1050       1055
      ATA   AAG   CCG   ATA   CTG   GGA   GAG   TAT   TAT   CAG   TTG   CAT   GGG   ACG   CCG   GTG
      TAT   TTC   GGC   TAT   GAC   CCT   CTC   ATA   ATA   GTC   AAC   GTA   CCC   TGC   GGC   CAC
       I     K     P     I     L     G     E     Y     Y     Q     L     H     G     T     P     V>

      1060  1065       1070       1075  1080       1085       1090  1095       1100
      GTT   AAG   GCG   ATG   TGC   AGG   GAG   GCC   AAG   GAG   TGT   ATC   TAT   GTG   GAA   CCG
      CAA   TTC   CGC   TAC   ACC   TCC   CTC   CGG   TTC   CTC   ACA   TAG   ATA   CAC   CTT   GGC
       V     K     A     M     W     R     E     A     K     E     C     I     Y     V     E     P>

      1105  1110       1115       1120  1125       1130       1135  1140       1145       1150
      GAC   AGG   CAA   GGT   GAG   AAG   AAA   GGT   CTC   TTC   TGG   TAC   AAC   AAT   AAG   TTA
      CTG   TCC   GTT   CCA   CTC   TTC   TTT   CCA   GAG   AAG   ACC   ATG   TTG   TTA   TTC   AAT
       D     R     Q     G     E     K     K     G     V     F     W     Y     N     N     K     L>

      1155       1160  1165  1170
      TGA   AGC   AAA   GAA   GAA   ACA   AT
      ACT   TCG   TTT   CTT   CTT   TGT   TA
       *     S     K     E     E     T     X>
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both strands
(see page 134)
for primer location

Total 5 independent
129 and 9508
clones (each with
Vm) were
sequenced by
primer DR
(see page 134)
and showed the
same mutations.
Thus it appears
to be true
mutation.
This will be
further confirmed
by re RT-PCR
RNA from 129 cells
and sequence by
DR primer

EXPERIMENTER _Geo R Mu_ DATE ____

WITNESSED BY _C. Sheppard_ DATE ____

DUPONT

AGRICULTURAL PRODUCTS
Experimental Station
P.O. Box 80402
Wilmington, Delaware 19880-0402

Mr. Ronald Lundquist
Fisher Richardson
330 Dain Bosworth Tower
60 S. 6th St.
Minneapolis, Minnesota 55402

Dear Ron:

It was very nice speaking with you over the phone on Monday. I am sending you the information about the molecular analysis of IMC129 and IMCQ508 mutations, which you requested for IMC129 and IMCQ508 patent application. A disc containing the nucleotide sequences for both canola FAD2 genes (D and F) are also included.

As we discussed over the phone, IMCQ508 mutation was identified based on sequencing of cDNA clones isolated from IMCQ508 mutant, however, the mutation had not been confirmed as we did for IMC129 mutation. Therefore, we might need to further confirm the mutation, if we would like to include IMCQ508 in the patent application. Please feel free to contact me if I can provide you any additional information about the two mutants.

Sincerely,

[signature]

Guo-Hua Miao, Ph.D.
Research Molecular Biologist

CC: W. R. Majarian

Encl.

```
        5    10        15   20        25   30        35   40        45   50
        *                   *                   *                   *                   *
ATGGGTGCAG GTGGAAGAAT GCAAGTGTCT CCTCCCTCCA AAAAGTCTGA
TACCCACGTC CACCTTCTTA CGTTCACAGA GGAGGGAGGT TTTTCAGACT


       55   60        65   70        75   80        85   90        95  100
        *                   *                   *                   *                   *
AACCGACAAC ATCAAGCGCG TACCCTGCGA GACACCGCCC TTCACTGTCG
TTGGCTGTTG TAGTTCGCGC ATGGGACGCT CTGTGGCGGG AAGTGACAGC


      105  110       115  120       125  130       135  140       145  150
        *                   *                   *                   *                   *
GAGAACTCAA GAAAGCAATC CCACCGCACT GTTTCAAACG CTCGATCCCT
CTCTTGAGTT CTTTCGTTAG GGTGGCGTGA CAAAGTTTGC GAGCTAGGGA


      155  160       165  170       175  180       185  190       195  200
        *                   *                   *                   *                   *
CGCTCTTTCT CCTACCTCAT CTGGGACATC ATCATAGCCT CCTGCTTCTA
GCGAGAAAGA GGATGGAGTA GACCCTGTAG TAGTATCGGA GGACGAAGAT


      205  210       215  220       225  230       235  240       245  250
        *                   *                   *                   *                   *
CTACGTCGCC ACCACTTACT TCCCTCTCCT CCCTCACCCT CTCTCCTACT
GATGCAGCGG TGGTGAATGA AGGGAGAGGA GGGAGTGGGA GAGAGGATGA


      255  260       265  270       275  280       285  290       295  300
        *                   *                   *                   *                   *
TCGCCTGGCC TCTCTACTGG GCCTGCCAGG GCTGCGTCCT AACCGGCGTC
AGCGGACCGG AGAGATGACC CGGACGGTCC CGACGCAGGA TTGGCCGCAG


      305  310       315  320       325  330       335  340       345  350
        *                   *                   *                   *                   *
TGGGTCATAG CCCACAGTG CGGCCACCAC GCCTTCAGCG ACTACCAGTG
ACCCAGTATC GGGTGTCAC GCCGGTGGTG CGGAAGTCGC TGATGGTCAC


      355  360       365  370       375  380       385  390       395  400
        *                   *                   *                   *                   *
GCTGGACGAC ACCGTCGGCC TCATCTTCCA CTCCTTCCTC CTCGTCCCTT
CGACCTGCTG TGGCAGCCGG AGTAGAAGGT GAGGAAGGAG GAGCAGGGAA


      405  410       415  420       425  430       435  440       445  450
        *                   *                   *                   *                   *
ACTTCTCCTG GAAGTACAGT CATCGACGCC ACCATTCCAA CACTGGCTCC
TGAAGAGGAC CTTCATGTCA GTAGCTGCGG TGGTAAGGTT GTGACCGAGG


      455  460       465  470       475  480       485  490       495  500
        *                   *                   *                   *                   *
CTCGAGAGAG ACGAAGTGTT TGTCCCCAAG AAGAAGTCAG ACATCAAGTG
GAGCTCTCTC TGCTTCACAA ACAGGGGTTC TTCTTCAGTC TGTAGTTCAC


      505  510       515  520       525  530       535  540       545  550
        *                   *                   *                   *                   *
GTACGGCAAG TACCCAACA ACCCTTTGGG ACGCACCGTG ATGTTAACGG
CATGCCGTTC ATGGGTTGT TGGGAAACCC TGCGTGGCAC TACAATTGCC


      555  560       565  570       575  580       585  590       595  600
        *                   *                   *                   *                   *
TTCAGTTCAC TCTCGGCTGG CCTTTGTACT TAGCCTTCAA CGTCTCGGGG
AAGTCAAGTG AGAGCCGACC GGAAACATGA ATCGGAAGTT GCAGAGCCCC


      605  610       615  620       625  630       635  640       645  650
        *                   *                   *                   *                   *
AGACCTTACG ACGGCGGCTT CGCTTGCCAT TTCCACCCCA ACGCTCCCAT
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          TCTGGAATGC TGCCGCCGAA GCGAACGGTA AAGGTGGGGT TGCGAGGGTA

            655  660   665  670   675  680   685  690   695  700
                   *          *          *          *          *
          CTACAACGAC CGCGAGCGTC TCCAGATATA CATCTCCGAC GCTGGCATCC
          GATGTTGCTG GCGCTCGCAG AGGTCTATAT GTAGAGGCTG CGACCGTAGG

            705  710   715  720   725  730   735  740   745  750
                   *          *          *          *          *
          TCGCCGTCTG CTACGGTCTC TACCGCTACG CTGCTGTCCA AGGAGTTGCC
          AGCGGCAGAC GATGCCAGAG ATGGCGATGC GACGACAGGT TCCTCAACGG

            755  760   765  770   775  780   785  790   795  800
                   *          *          *          *          *
          TCGATGGTCT GCTTCTACGG AGTTCCGCTT CTGATTGTCA ATGGGTTCTT
          AGCTACCAGA CGAAGATGCC TCAAGGCGAA GACTAACAGT TACCCAAGAA

            805  810   815  820   825  830   835  840   845  850
                   *          *          *          *          *
          AGTTTTGATC ACTTACTTGC AGCACACGCA TCCTTCCCTG CCTCACTATG
          TCAAAACTAG TGAATGAACG TCGTGTGCGT AGGAAGGGAC GGAGTGATAC

            855  860   865  870   875  880   885  890   895  900
                   *          *          *          *          *
          ACTCGTCTGA GTGGGATTGG TTGAGGGGAG CTTTGGCCAC CGTTGACAGA
          TGAGCAGACT CACCCTAACC AACTCCCCTC GAAACCGGTG GCAACTGTCT

            905  910   915  920   925  930   935  940   945  950
                   *          *          *          *          *
          GACTACGGAA TCTTGAACAA GGTCTTCCAC AATATCACGG ACACGCACGT
          CTGATGCCTT AGAACTTGTT CCAGAAGGTG TTATAGTGCC TGTGCGTGCA

            955  960   965  970   975  980   985  990   995 1000
                   *          *          *          *          *
          GGCGCATCAC CTGTTCTCGA CCATGCCGCA TTATCATGCG ATGGAAGCTA
          CCGCGTAGTG GACAAGAGCT GGTACGGCGT AATAGTACGC TACCTTCGAT

           1005 1010  1015 1020  1025 1030  1035 1040  1045 1050
                   *          *          *          *          *
          CGAAGGCGAT AAAGCCGATA CTGGGAGAGT ATTATCAGTT GCATGGGACG
          GCTTCCGCTA TTTCGGCTAT GACCCTCTCA TAATAGTCAA CGTACCCTGC

           1055 1060  1065 1070  1075 1080  1085 1090  1095 1100
                   *          *          *          *          *
          CCGGTGGTTA AGGCGATGTG GAGGGAGGCG AAGGAGTGTA TCTATGTGGA
          GGCCACCAAT TCCGCTACAC CTCCCTCCGC TTCCTCACAT AGATACACCT

           1105 1110  1115 1120  1125 1130  1135 1140  1145 1150
                   *          *          *          *          *
          ACCGGACAGG CAAGGTGAGA AGAAAGGTGT GTTCTGGTAC AACAATAAGT
          TGGCCTGTCC GTTCCACTCT TCTTTCCACA CAAGACCATG TTGTTATTCA

           1155 1160  1165 1170
                   *          *
          TATGAAGCAA AGAAGAAACA AT
          ATACTTCGTT TCTTCTTTGT TA
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Sequence Range: 1 to 1172

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        5        10       15        20       25        30       35        40       45
         *                 *                  *                  *
ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAA AAG TCT
TAC CCA CGT CCA CCT TCT TAC GTT CAC AGA GGA GGG AGG TTT TTC AGA
 M   G   A   G   G   R   M   Q   V   S   P   P   S   K   K   S>

 50       55       60        65       70   75        80       85       90        95
  *                 *                  *                  *                  *
GAA ACC GAC AAC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT
CTT TGG CTG TTG TAG TTC GCG CAT GGG ACG CTC TGT GGC GGG AAG TGA
 E   T   D   N   I   K   R   V   P   C   E   T   P   P   F   T>

      100  105      110      115      120      125      130  135      140
       *             *                  *                  *             *
GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG
CAG CCT CTT GAG TTC TTT CGT TAG GGT GGC GTG ACA AAG TTT GCG AGC
 V   G   E   L   K   K   A   I   P   P   H   C   F   K   R   S>

 145  150      155      160      165      170      175      180      185      190
       *                 *                  *                  *                  *
ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC
TAG GGA GCG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAG TAT CGG AGG
 I   P   R   S   F   S   Y   L   I   W   D   I   I   I   A   S>

 195      200      205      210      215      220      225      230      235      240
            *                 *                  *                  *                  *
TGC TTC TAC TAC GTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT
ACG AAG ATG ATG CAG CGG TGG TGA ATG AAG GGA GAG GAG GGA GTG GGA
 C   F   Y   Y   V   A   T   T   Y   F   P   L   L   P   H   P>

      245      250      255      260      265      270      275      280      285
            *                 *                  *                  *
CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAG GGC TGC GTC
GAG AGG ATG AAG CGG ACC GGA GAG ATG ACC CGG ACG GTC CCG ACG CAG
 L   S   Y   F   A   W   P   L   Y   W   A   C   Q   G   C   V>

 290      295      300      305      310      315      320      325      330      335
            *                 *                  *                  *                  *
CTA ACC GGC GTC TGG GTC ATA GCC CAC GAG TGC GGC CAC CAC GCC TTC
GAT TGG CCG CAG ACC CAG TAT CGG GTG CTC ACG CCG GTG GTG CGG AAG
 L   T   G   V   W   V   I   A   H   E   C   G   H   H   A   F>

      340      345      350      355      360      365      370      375      380
       *                 *                  *                  *                  *
AGC GAC TAC CAG TGG CTG GAC GAC ACC GTC GGC CTC ATC TTC CAC TCC
TCG CTG ATG GTC ACC GAC CTG CTG TGG CAG CCG GAG TAG AAG GTG AGG
 S   D   Y   Q   W   L   D   D   T   V   G   L   I   F   H   S>

 385  390      395      400      405      410      415      420      425      430
            *                 *                  *                  *                  *
TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGA CGC CAC
AAG GAG GAG CAG GGA ATG AAG AGG ACC TTC ATG TCA GTA GCT GCG GTG
 F   L   L   V   P   Y   F   S   W   K   Y   S   H   R   R   H>

 435  440      445      450      455      460      465      470      475      480
            *                 *                  *                  *                  *
CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG
GTA AGG TTG TGA CCG AGG GAG CTC TCT CTG CTT CAC AAA CAG GGG TTC
 H   S   N   T   G   S   L   E   R   D   E   V   F   V   P   K>
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f-gene, 508 Translated Sequence
3:53 AM
(found in Wild type + 129 F gene)
Page 2

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        485     490     495     500     505     510     515     520     525
                 *               *               *               *
        AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CAC AAC AAC CCT TTG
        TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GTG TTG TTG GGA AAC
         K   K   S   D   I   K   W   Y   G   K   Y   H   N   N   P   L>

        530     535     540     545     550     555     560     565     570     575
         *               *               *               *               *
        GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCT TTG
        CCT GCG TGG CAC TAC AAT TGC CAA GTC AAG TGA GAG CCG ACC GGA AAC
         G   R   T   V   M   L   T   V   Q   F   T   L   G   W   P   L>

            580     585     590     595     600     605     610     615     620
             *               *               *               *               *
        TAC TTA GCC TTC AAC GTC TCG GGG AGA CCT TAC GAC GGC GGC TTC GCT
        ATG AAT CGG AAG TTG CAG AGC CCC TCT GGA ATG CTG CCG CCG AAG CGA
         Y   L   A   F   N   V   S   G   R   P   Y   D   G   G   F   A>

        625     630     635     640     645     650     655     660     665     670
                 *               *               *               *               *
        TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC
        ACG GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG
         C   H   F   H   P   N   A   P   I   Y   N   D   R   E   R   L>

            675     680     685     690     695     700     705     710     715     720
                     *               *               *               *               *
        CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC
        GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CGG CAG ACG ATG CCA GAG
         Q   I   Y   I   S   D   A   G   I   L   A   V   C   Y   G   L>

            725     730     735     740     745     750     755     760     765
                     *               *               *               *
        TAC CGC TAC GCT GCT GTC CAA GGA GTT GCC TCG ATG GTC TGC TTC TAC
        ATG GCG ATG CGA CGA CAG GTT CCT CAA CGG AGC TAC CAG ACG AAG ATG
         Y   R   Y   A   A   V   Q   G   V   A   S   M   V   C   F   Y>

        770     775     780     785     790     795     800     805     810     815
         *               *               *               *               *
        GGA GTT CCG CTT CTG ATT GTC AAT GGG TTC TTA GTT TTG ATC ACT TAC
        CCT CAA GGC GAA GAC TAA CAG TTA CCC AAG AAT CAA AAC TAG TGA ATG
         G   V   P   L   L   I   V   N   G   F   L   V   L   I   T   Y>

            820     825     830     835     840     845     850     855     860
             *               *               *               *               *
        TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAT GAC TCG TCT GAG TGG
        AAC GTC GTG TGC GTA GGA AGG GAC GGA GTG ATA CTG AGC AGA CTC ACC
         L   Q   H   T   H   P   S   L   P   H   Y   D   S   S   E   W>

        865     870     875     880     885     890     895     900     905     910
                 *               *               *               *               *
        GAT TGG TTG AGG GGA GCT TTG GCC ACC GTT GAC AGA GAC TAC GGA ATC
        CTA ACC AAC TCC CCT CGA AAC CGG TGG CAA CTG TCT CTG ATG CCT TAG
         D   W   L   R   G   A   L   A   T   V   D   R   D   Y   G   I>

        915     920     925     930     935     940     945     950     955     960
                 *               *               *               *               *
        TTG AAC AAG GTC TTC CAC AAT ATC ACG GAC ACG CAC GTG GCG CAT CAC
        AAC TTG TTC CAG AAG GTG TTA TAG TGC CTG TGC GTG CAC CGC GTA GTG
         L   N   K   V   F   H   N   I   T   D   T   H   V   A   H   H>

            965     970     975     980     985     990     995    1000    1005
                     *               *               *               *
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     CTG TTC TCG ACC ATG CCG CAT TAT CAT GCG ATG GAA GCT ACG AAG GCG
     GAC AAG AGC TGG TAC GGC GTA ATA GTA CGC TAC CTT CGA TGC TTC CGC
      L   F   S   T   M   P   H   Y   H   A   M   E   A   T   K   A>

     1010   1015  1020   1025   1030 1035   1040   1045 1050   1055
       *            *            *            *            *

     ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTG CAT GGG ACG CCG GTG
     TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAC GTA CCC TGC GGC CAC
      I   K   P   I   L   G   E   Y   Y   Q   L   H   G   T   P   V>

        1060 1065   1070  1075 1080   1085   1090 1095   1100
          *            *            *            *            *

     GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG
     CAA TTC CGC TAC ACC TCC CTC CGC TTC CTC ACA TAG ATA CAC CTT GGC
      V   K   A   M   W   R   E   A   K   E   C   I   Y   V   E   P>

     1105 1110   1115   1120 1125   1130   1135 1140   1145   1150
            *            *            *            *            *

     GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA
     CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT
      D   R   Q   G   E   K   K   G   V   F   W   Y   N   N   K   L>

     1155   1160   1165 1170
              *            *

     TGA AGC AAA GAA GAA ACA AT
     ACT TCG TTT CTT CTT TGT TA
      *   S   K   E   E   T   X>
```

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         5    10        15   20        25   30        35   40        45   50
         *                   *                   *                   *                   *
    ATGGGTGCAG GTGGAAGAAT GCAAGTGTCT CCTCCCTCCA AGAAGTCTGA
    TACCCACGTC CACCTTCTTA CGTTCACAGA GGAGGGAGGT TCTTCAGACT

        55   60        65   70        75   80        85   90        95  100
         *                   *                   *                   *                   *
    AACCGACACC ATCAAGCGCG TACCCTGCGA GACACCGCCC TTCACTGTCG
    TTGGCTGTGG TAGTTCGCGC ATGGGACGCT CTGTGGCGGG AAGTGACAGC

       105  110       115  120       125  130       135  140       145  150
         *                   *                   *                   *                   *
    GAGAACTCAA GAAAGCAATC CCACCGCACT GTTTCAAACG CTCGATCCCT
    CTCTTGAGTT CTTTCGTTAG GGTGGCGTGA CAAAGTTTGC GAGCTAGGGA

       155  160       165  170       175  180       185  190       195  200
         *                   *                   *                   *                   *
    CGCTCTTTCT CCTACCTCAT CTGGGACATC ATCATAGCCT CCTGCTTCTA
    GCGAGAAAGA GGATGGAGTA GACCCTGTAG TAGTATCGGA GGACGAAGAT

       205  210       215  220       225  230       235  240       245  250
         *                   *                   *                   *                   *
    CTACNTCGCC ACCACTTACT TCCCTCTCCT CCCTCACCCT CTCTCCTACT
    GATGNAGCGG TGGTGAATGA AGGGAGAGGA GGGAGTGGGA GAGAGGATGA

       255  260       265  270       275  280       285  290       295  300
         *                   *                   *                   *                   *
    TCGCCTGGCC TCTCTACTGG GCCTGCCAAG GGTGCGTCCT AACCGGCGTC
    AGCGGACCGG AGAGATGACC CGGACGGTTC CCACGCAGGA TTGGCCGCAG

                                    G (in wild type D gene)
       305  310       315 G 320       325 √330       335) 340       345  350
         *                   *                   *                   *                   *
    TGGGTCATAG CCCAC↓AGTG CGGCCACCAC GCCTTCAGCG ACTACCAGTG
    ACCCAGTATC GGGTG↑TCAC GCCGGTGGTG CGGAAGTCGC TGATGGTCAC

       355  360       365  370       375  380       385  390       395  400
         *                   *                   *                   *                   *
    GCTTGACGAC ACCGTCGGTC TCATCTTCCA CTCCTTCCTC CTCGTCCCTT
    CGAACTGCTG TGGCAGCCAG AGTAGAAGGT GAGGAAGGAG GAGCAGGGAA

       405  410       415  420       425  430       435  440       445  450
         *                   *                   *                   *                   *
    ACTTCTCCTG GAAGTACAGT CATCGCAGCC ACCATTCCAA CACTGGCTCC
    TGAAGAGGAC CTTCATGTCA GTAGCGTCGG TGGTAAGGTT GTGACCGAGG

       455  460       465  470       475  480       485  490       495  500
         *                   *                   *                   *                   *
    CTCGAGAGAG ACGAAGTGTT TGTCCCCAAG AAGAAGTCAG ACATCAAGTG
    GAGCTCTCTC TGCTTCACAA ACAGGGGTTC TTCTTCAGTC TGTAGTTCAC

       505  510       515  520       525  530       535  540       545  550
         *                   *                   *                   *                   *
    GTACGGCAAG TACCTCAACA ACCCTTTGGG ACGCACCGTG ATGTTAACGG
    CATGCCGTTC ATGGAGTTGT TGGGAAACCC TGCGTGGCAC TACAATTGCC

       555  560       565  570       575  580       585  590       595  600
         *                   *                   *                   *                   *
    TTCAGTTCAC TCTCGGCTGG CCGTTGTACT TAGCCTTCAA CGTCTCGGGA
    AAGTCAAGTG AGAGCCGACC GGCAACATGA ATCGGAAGTT GCAGAGCCCT

       605  610       615  620       625  630       635  640       645  650
         *                   *                   *                   *                   *
    AGACCTTACG ACGGCGGCTT CCGTTGCCAT TTCCACCCCA ACGCTCCCAT
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TCTGGAATGC TGCCGCCGAA GGCAACGGTA AAGGTGGGGT TGCGAGGGTA

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      655   660     665   670     675   680     685   690     695   700
        *             *             *             *             *
CTACAACGAC CGCGAGCGTC TCCAGATATA CATCTCCGAC GCTGGCATCC
GATGTTGCTG GCGCTCGCAG AGGTCTATAT GTAGAGGCTG CGACCGTAGG

      705   710     715   720     725   730     735   740     745   750
        *             *             *             *             *
TCGCCGTCTG CTACGGTCTC TTCCGTTACG CCGCCGGCCA GGGAGTGGCC
AGCGGCAGAC GATGCCAGAG AAGGCAATGC GGCGGCCGGT CCCTCACCGG

      755   760     765   770     775   780     785   790     795   800
        *             *             *             *             *
TCGATGGTCT GCTTCTACGG AGTCCCGCTT CTGATTGTCA ATGGTTTCCT
AGCTACCAGA CGAAGATGCC TCAGGGCGAA GACTAACAGT TACCAAAGGA

      805   810     815   820     825   830     835   840     845   850
        *             *             *             *             *
CGTGTTGATC ACTTACTTGC AGCACACGCA TCCTTCCCTG CCTCACTACG
GCACAACTAG TGAATGAACG TCGTGTGCGT AGGAAGGGAC GGAGTGATGC

      855   860     865   870     875   880     885   890     895   900
        *             *             *             *             *
ATTCGTCCGA GTGGGATTGG TTCAGGGGAG CTTTGGCTAC CGTTGACAGA
TAAGCAGGCT CACCCTAACC AAGTCCCCTC GAAACCGATG GCAACTGTCT

      905   910     915   920     925   930     935   940     945   950
        *             *             *             *             *
GACTACGGAA TCTTGAACAA GGTCTTCCAC AATATTACCG ACACGCACGT
CTGATGCCTT AGAACTTGTT CCAGAAGGTG TTATAATGGC TGTGCGTGCA

      955   960     965   970     975   980     985   990     995  1000
        *             *             *             *             *
GGCCCATCAT CCGTTCTCCA CGATGCCGCA TTATCACGCG ATGGAAGCTA
CCGGGTAGTA GGCAAGAGGT GCTACGGCGT AATAGTGCGC TACCTTCGAT

     1005  1010    1015  1020    1025  1030    1035  1040    1045  1050
        *             *             *             *             *
CCAAGGCGAT AAAGCCGATA CTGGGAGAGT ATTATCAGTT CGATGGGACG
GGTTCCGCTA TTTCGGCTAT GACCCTCTCA TAATAGTCAA GCTACCCTGC

     1055  1060    1065  1070    1075  1080    1085  1090    1095  1100
        *             *             *             *             *
CCGGTGGTTA AGGCGATGTG GAGGGAGGCG AAGGAGTGTA TCTATGTGGA
GGCCACCAAT TCCGCTACAC CTCCCTCCGC TTCCTCACAT AGATACACCT

     1105  1110    1115  1120    1125  1130    1135  1140    1145  1150
        *             *             *             *             *
ACCGGACAGG CAAGGTGAGA AGAAAGGTGT GTTCTGGTAC AACAATAAGT
TGGCCTGTCC GTTCCACTCT TCTTTCCACA CAAGACCATG TTGTTATTCA

     1155  1160    1165  1170    1175  1180    1185
        *             *             *
TATGAGGATA TGATGATGGT GAAAGAAATC ACTAG
ATACTCCTAT ACTACTACCA CTTTCTTTAG TGATC
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Sequence Range: 1 to 1185

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              5        10       15        20       25       30        35        40       45
                       *                 *                 *                   *
         ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT
         TAC CCA CGT CCA CCT TCT TAC GTT CAC AGA GGA GGG AGG TTC TTC AGA
          M   G   A   G   G   R   M   Q   V   S   P   P   S   K   K   S>

        50       55       60       65       70       75       80       85       90       95
         *                 *                 *                 *                 *
         GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT
         CTT TGG CTG TGG TAG TTC GCG CAT GGG ACG CTC TGT GGC GGG AAG TGA
          E   T   D   T   I   K   R   V   P   C   E   T   P   P   F   T>

           100      105      110      115      120      125      130      135      140
            *                 *                 *                 *                 *
         GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG
         CAG CCT CTT GAG TTC TTT CGT TAG GGT GGC GTG ACA AAG TTT GCG AGC
          V   G   E   L   K   K   A   I   P   P   H   C   F   K   R   S>

        145      150      155      160      165      170      175      180      185      190
                   *                 *                 *                 *                 *
         ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC
         TAG GGA GCG AGA AAG AGG ATG GAG TAG ACC CTG TAG TAG TAT CGG AGG
          I   P   R   S   F   S   Y   L   I   W   D   I   I   I   A   S>

          195      200      205      210      215      220      225      230      235      240
                    *                 *                 *                 *                 *
         TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT
         ACG AAG ATG ATG NAG CGG TGG TGA ATG AAG GGA GAG GAG GGA GTG GGA
          C   F   Y   Y   X   A   T   T   Y   F   P   L   L   P   H   P>

              245      250      255      260      265      270      275      280      285
                        *                 *                 *                 *
         CTC TCC TAC TTC GCC TGG CCT CTC TAC TGG GCC TGC CAA GGG TGC GTC
         GAG AGG ATG AAG CGG ACC GGA GAG ATG ACC CGG ACG GTT CCC ACG CAG
          L   S   Y   F   A   W   P   L   Y   W   A   C   Q   G   C   V>

         290      295      300      305      310      315      320      325      330      335
                             *                 *                 *                 *
         CTA ACC GGC GTC TGG GTC ATA GCC CAC AAG TGC GGC CAC CAC GCC TTC
         GAT TGG CCG CAG ACC CAG TAT CGG GTG TTC ACG CCG GTG GTG CGG AAG
          L   T   G   V   W   V   I   A   H   K   C   G   H   H   A   F>

            340      345      350      355      360      365      370      375      380
                   *                 *                 *                 *                 *
         AGC GAC TAC CAG TGG CTT GAC GAC ACC GTC GGT CTC ATC TTC CAC TCC
         TCG CTG ATG GTC ACC GAA CTG CTG TGG CAG CCA GAG TAG AAG GTG AGG
          S   D   Y   Q   W   L   D   D   T   V   G   L   I   F   H   S>

        385      390      395      400      405      410      415      420      425      430
                   *                 *                 *                 *                 *
         TTC CTC CTC GTC CCT TAC TTC TCC TGG AAG TAC AGT CAT CGC AGC CAC
         AAG GAG GAG CAG GGA ATG AAG AGG ACC TTC ATG TCA GTA GCG TCG GTG
          F   L   L   V   P   Y   F   S   W   K   Y   S   H   R   S   H>

        435      440      445      450      455      460      465      470      475      480
                   *                 *                 *                 *                 *
         CAT TCC AAC ACT GGC TCC CTC GAG AGA GAC GAA GTG TTT GTC CCC AAG
         GTA AGG TTG TGA CCG AGG GAG CTC TCT CTG CTT CAC AAA CAG GGG TTC
          H   S   N   T   G   S   L   E   R   D   E   V   F   V   P   K>
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            485      490      495      500      505      510      515      520      525
              *               *                 *                 *
         AAG AAG TCA GAC ATC AAG TGG TAC GGC AAG TAC CTC AAC AAC CCT TTG
         TTC TTC AGT CTG TAG TTC ACC ATG CCG TTC ATG GAG TTG TTG GGA AAC
          K   K   S   D   I   K   W   Y   G   K   Y   L   N   N   P   L>

         530      535      540      545      550      555      560      565      570      575
          *                *                *                 *                 *
         GGA CGC ACC GTG ATG TTA ACG GTT CAG TTC ACT CTC GGC TGG CCG TTG
         CCT GCG TGG CAC TAC AAT TGC CAA GTC AAG TGA GAG CCG ACC GGC AAC
          G   R   T   V   M   L   T   V   Q   F   T   L   G   W   P   L>

            580      585      590      595      600      605      610      615      620
              *                *                *                 *                 *
         TAC TTA GCC TTC AAC GTC TCG GGA AGA CCT TAC GAC GGC GGC TTC CGT
         ATG AAT CGG AAG TTG CAG AGC CCT TCT GGA ATG CTG CCG CCG AAG GCA
          Y   L   A   F   N   V   S   G   R   P   Y   D   G   G   F   R>

         625      630      635      640      645      650      655      660      665      670
                   *                *                *                 *                 *
         TGC CAT TTC CAC CCC AAC GCT CCC ATC TAC AAC GAC CGC GAG CGT CTC
         ACG GTA AAG GTG GGG TTG CGA GGG TAG ATG TTG CTG GCG CTC GCA GAG
          C   H   F   H   P   N   A   P   I   Y   N   D   R   E   R   L>

            675      680      685      690      695      700      705      710      715      720
                     *                *                *                 *                 *
         CAG ATA TAC ATC TCC GAC GCT GGC ATC CTC GCC GTC TGC TAC GGT CTC
         GTC TAT ATG TAG AGG CTG CGA CCG TAG GAG CGG CAG ACG ATG CCA GAG
          Q   I   Y   I   S   D   A   G   I   L   A   V   C   Y   G   L>

            725      730      735      740      745      750      755      760      765
                      *                *                *                 *
         TTC CGT TAC GCC GCC GGC CAG GGA GTG GCC TCG ATG GTC TGC TTC TAC
         AAG GCA ATG CGG CGG CCG GTC CCT CAC CGG AGC TAC CAG ACG AAG ATG
          F   R   Y   A   A   G   Q   G   V   A   S   M   V   C   F   Y>

         770      775      780      785      790      795      800      805      810      815
          *                *                *                 *                 *
         GGA GTC CCG CTT CTG ATT GTC AAT GGT TTC CTC GTG TTG ATC ACT TAC
         CCT CAG GGC GAA GAC TAA CAG TTA CCA AAG GAG CAC AAC TAG TGA ATG
          G   V   P   L   L   I   V   N   G   F   L   V   L   I   T   Y>

            820      825      830      835      840      845      850      855      860
              *                *                *                 *                 *
         TTG CAG CAC ACG CAT CCT TCC CTG CCT CAC TAC GAT TCG TCC GAG TGG
         AAC GTC GTG TGC GTA GGA AGG GAC GGA GTG ATG CTA AGC AGG CTC ACC
          L   Q   H   T   H   P   S   L   P   H   Y   D   S   S   E   W>

         865      870      875      880      885      890      895      900      905      910
                   *                *                *                 *                 *
         GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC
         CTA ACC AAG TCC CCT CGA AAC CGA TGG CAA CTG TCT CTG ATG CCT TAG
          D   W   F   R   G   A   L   A   T   V   D   R   D   Y   G   I>

         915      920      925      930      935      940      945      950      955      960
                   *                *                *                 *                 *
         TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT
         AAC TTG TTC CAG AAG GTG TTA TAA TGG CTG TGC GTG CAC CGG GTA GTA
          L   N   K   V   F   H   N   I   T   D   T   H   V   A   H   H>

            965      970      975      980      985      990      995     1000    1005
                      *                *                *                 *
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CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG
GGC AAG AGG TGC TAC GGC GTA ATA GTG CGC TAC CTT CGA TGG TTC CGC
 P   F   S   T   M   P   H   Y   H   A   M   E   A   T   K   A>

  1010   1015 1020    1025    1030 1035    1040    1045 1050    1055
     *              *               *             *             *
ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG
TAT TTC GGC TAT GAC CCT CTC ATA ATA GTC AAG CTA CCC TGC GGC CAC
 I   K   P   I   L   G   E   Y   Y   Q   F   D   G   T   P   V>

    1060 1065    1070 1075 1080    1085    1090 1095    1100
       *             *               *             *
GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG
CAA TTC CGC TAC ACC TCC CTC CGC TTC CTC ACA TAG ATA CAC CTT GGC
 V   K   A   M   W   R   E   A   K   E   C   I   Y   V   E   P>

1105 1110    1115    1120 1125    1130    1135 1140    1145    1150
        *               *               *             *             *
GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA
CTG TCC GTT CCA CTC TTC TTT CCA CAC AAG ACC ATG TTG TTA TTC AAT
 D   R   Q   G   E   K   K   G   V   F   W   Y   N   N   K   L>

  1155    1160    1165 1170    1175    1180 1185
             *             *             *
TGA GGA TAT GAT GAT GGT GAA AGA AAT CAC TAG
ACT CCT ATA CTA CTA CCA CTT TCT TTA GTG ATC
 *   G   Y   D   D   G   E   R   N   H   *>
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